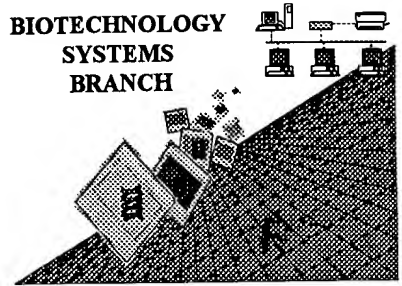


T. Scheiner

RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



SCIENTIFIC AND TECHNICAL INFORMATION CENTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

08/974,584

Art Unit / Team No. :

1642

Date Processed by STIC:

12/22/98

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/974,584DATE: 12/22/98
TIME: 09:59:37

INPUT SET: S30432.raw

RECEIVED

This Raw Listing contains the General
Information Section and up to the first 5 pages.

APR 25 2000
TECH CENTER 1600/2900Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

(ii) TITLE OF INVENTION: Telomerase Reverse Transcriptase

(iii) NUMBER OF SEQUENCES: 482

see p. 3

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Townsend and Townsend and Crew LLP
(B) STREET: Two Embarcadero Center, Eighth Floor
(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94111-3834

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/974,584
(B) FILING DATE: 19-NOV-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/724,643
(B) FILING DATE: 01-OCT-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/844,419
(B) FILING DATE: 18-APR-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/846,017
(B) FILING DATE: 25-APR-1997

08/974,584

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

Pro Gln Asn Pro Lys Thr Pro Lys Pro Leu
1 5 10
Arg 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240
Leu Ile Trp Met Ile Lys Ile Tyr Phe Leu Ile His Ser Thr Ser
Ile Ala Ala Leu Val Val Thr Arg Lys Asp Ala Lys His Cys Asn Leu
Ala Arg Asn Arg Leu His Cys Leu Phe Gln Ser Cys Lys Asn Asn
Ser Ser Thr Ser Arg Met Gln Ile Phe Ile Thr Ile Leu Ser Cys Glu
Asn Phe Lys Ala Glu Ser Lys Glu Lys Leu Lys His Tyr
Cys Leu Asn Lys Ile Arg Cys Gly Leu Phe Tyr Phe Leu Asp
His Phe Leu Arg Ser Ile Met Glu Lys Ile Thr Tyr Lys Val
Asn Ser Leu Asp Tyr Phe Pro Ser Gln Gln Cys Cys Val Tyr Ile
His Met Arg Met Ser Gln Arg Ile Ser Ile His Gln Thr Tyr Gln Arg
Gln Thr Arg Tyr Lys Thr Gln Glu Lys Val Cys Ser Asn Ser Arg
Arg Thr Tyr Cys Ile Tyr Tyr Ser Tyr Gly Phe Tyr Tyr Asn Cys Phe
Arg Tyr Arg Arg Cys Thr Pro Glu Ser Cys Asp Asn Cys Lys Ser Cys
Leu Gln Leu Lys Glu Ser Gln Phe Cys Lys Phe Cys Cys Val Cys His
Tyr Phe Val Asn Ser Gln Ile Ser Tyr Leu Asn Leu Met Asp Ser

all
groups of
4 or more
amino acids
following
a stop
codon (*)
need their
own SEQ
ID NO.

Please
re-number
the amino
acid and
adjust
the sequence
to

(iii) NUMBER OF
SEQUENCES:
on p. 1.
to include
the new
sequences

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245

250

255

Tyr Arg Asn Lys Pro Asn Lys Pro Cys Lys Phe Asn Gly Ile Tyr Val
 260 265 270

Lys Ser Phe Gly Thr Asn Ala His Cys Ile Tyr Ile Gly Phe Leu Lys
 275 280 285

His Arg Tyr Thr Glu Cys Phe Arg Asp Cys Phe Ser Leu Gln Gln Ile
 290 295 300

Thr Cys Phe Asp Tyr Ser Cys Ser Ser Leu Ile Ser Leu Lys Glu Ala
 305 310 315 320

Gly Glu Met Lys Arg Arg Leu Lys Lys Glu Ile Ser Lys Phe Val Asp
 325 330 335

Ser Ser Val Thr Gly Ile Asn Asn Lys Asn Ile Ser Asn Glu Lys Glu
 340 345 350

Glu Glu Leu Ser Gln Ser Cys Phe Leu Lys Ile Ser Lys Ile Pro Gly
 355 360 365

Lys Arg Asp Thr Phe Ile Lys Ile His Ile Leu] * [Phe Phe Ile Ser
 370 375 380 *new SEQ ID NO.*

Gln Leu Leu Phe Ser Phe Ile Leu Thr Ile Phe Phe Asp] * [Leu Glu
 385 390 395 400 *new SEQ ID NO.*

Val Lys Ser Ile Lys] * [~~Glu Lys Arg~~ * [Thr Glu Val Thr] * [Leu
 405 410 415 *new SEQ ID NO.*

Ile His Ile His Arg Ser Thr Phe Ile Tyr Pro Ile Arg Cys] * [Gly
 420 425 430 *new SEQ ID NO.*

Asn Ser Ser His Pro Phe] * [~~Lys~~ * [Cys Tyr Glu Asp] * [Ile Phe
 435 440 445 *new SEQ ID NO.*

Arg Val Lys Lys Trp Ser Arg Asn Leu Asn Gln Lys Glu Leu Arg Arg
 450 455 460

Tyr Cys Lys Arg Ile Glu Leu] * [~~Ile Phe Arg~~ * [Val Leu Pro
 465 470 475 480 *new SEQ ID NO.*

Ile Leu Ile Asp Cys Arg Asp Cys Arg Gly Asn Cys Thr Glu Asp His]
 485 490 495

(*) [Arg *new SEQ ID NO.* Lys Val Thr Phe Ile Asn] * [Arg Ile Asn] * [Ile Thr
 500 505 510 *new SEQ ID NO.*

Asn Ile Glu Ile Ser Asp Leu Gln Leu Thr Lys] * [~~Lys Leu Asn~~
 515 520 525

~~Ser~~ * [Thr Ile *new SEQ ID NO.* Lys Asn Thr Asn Leu Gly Gln Asn Ile Glu Glu Gly
 530 535 540

Lys Glu Asp Gln Leu Ala Lys Glu Lys Ile Arg Gln] * [Ile Lys Cys
new SEQ ID NO.

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545 Val Gln Lys Cys Arg Asn Lys Arg Phe Ile Phe Phe Asn Asn Leu Leu
565 570 575
Lys Arg Gly Val Leu Gly Phe Trp Gly Phe Gly }
580 585

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS: 15
(A) LENGTH: 587 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Pro Lys Thr Pro Lys Pro Gln Asn Pro Tyr Lys Lys Arg Lys Asn (*)
1 5 10 15
[Gly Ser Leu ^{new SEQ ID NO.} Glu Ile Lys Tyr Tyr Ser Arg Thr Asn Gly Asp Gly Tyr]
20 25 30
* ~~Phe Gly~~ (*) [Tyr Arg Lys Phe Thr Ser] (*) [Tyr Ile Gln Gln Val]
35 40 45
* ~~Gln Leu Leu~~ (*) [Gln ^{new SEQ ID NO.} Glu Arg Met Gln Asn Ile Glu Ile Trp]
50 55 60
Leu Glu Ile Ala Phe Ile Asp Tyr Ser Lys Val Ala Lys Thr Ile Arg
65 70 75 80
Val Leu Leu Leu Gly Cys Lys Ser Leu (*) [Arg ^{new SEQ ID NO.} Phe Phe Leu Glu Lys]
85 90 95
Ile Ser Phe Lys Lys Arg Arg Ala Lys Ser Arg Asn (*) [Asn ^{new SEQ ID NO.} Ile Thr]
100 105 110
Asn Val (*) [Ile ^{new SEQ ID NO.} Lys Ser Gly Asn Glu Asp Tyr Ser Ile Phe] (*) Ile
115 120 125
Thr Ser (*) [Gly ^{new SEQ ID NO.} Ala Leu Trp Arg Lys Leu Leu Asn Thr Lys Arg] (*)
130 135 140
[Thr Val Trp Ile ^{new SEQ ID NO.} Ile Ser Leu Ala Asn Asn Asp Glu Tyr Ile Lys Phe]
145 150 155 160
Ile (*) ~~Glu~~ (*) [Val ^{new SEQ ID NO.} Lys Gly Ser Arg Tyr Ile Arg Leu Thr Lys Asp]
165 170 175
Lys Leu Ala Ile Lys Arg Lys Lys Lys Phe Asp Asn Arg Thr Ala Glu
180 185 190
Glu Leu Ile Ala Phe Thr Ile Arg Met Gly Phe Ile Thr Ile Val Leu

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195

200

205

Gly Ile Asp Gly Glu Leu Pro Ser Leu Glu Thr Ile Glu Lys Ala Val
 210 215 220

Tyr Asn } (*) [Arg Asn Arg Ser Ser Glu Ser Ser Asp Val Tyr Ala Ile
 225 230 235 240

Ile Leu } (*) [Ile Asn Leu Lys Tyr Leu Ile Ser Ile } (*) [Trp Ile Ala
 245 250 255

Ile Glu Thr Asn Gln Ile Asn His Ala Ser Leu Met Glu Tyr Thr Leu
 260 265 270

Asn Pro Leu Gly Gln Met His Thr Glu Phe Ile Leu Asp Ser } (*) [Ser
 275 280 285

Ile Asp Thr Gln Asn Ala Leu Glu Thr Asp Leu Ala Tyr Asn Arg Leu
 290 295 300

Pro Val Leu Ile Thr Leu Ala His Leu Leu Tyr Leu } (*) [Lys Lys Gln
 305 310 315 320

Ala Lys } (*) [Lys Glu Asp } (*) [Arg Lys Arg Phe Gln Asn Leu Leu Ile
 325 330 335

Leu Leu } (*) [Pro Glu Leu Thr Thr Arg Ile Leu Ala Thr Lys Lys Lys
 340 345 350

Lys Ser Tyr His Asn Pro Asp Ser } (*) [Arg Phe Gln Lys Phe Gln Val
 355 360 365

Arg Glu Ile His Ser Leu Lys Phe Ile Tyr Tyr Ser Phe Ser Phe His
 370 375 380

Ser Cys Tyr Phe Leu Leu Ser } (*) [Gln Tyr Phe Leu Ile Ser Trp Lys
 385 390 395 400

(*) [Lys Val Ser Asn Lys Arg Ser Ala Arg Leu Arg } (*) [Leu Ser Leu
 405 410 415

Phe Thr Phe Ile Asp Arg Pro Ser Tyr Ile Gln Tyr Asp Asp Lys Glu
 420 425 430

Thr Ala Val Ile Arg Phe Lys Asn Ser Ala Met Arg Thr Lys Phe Leu
 435 440 445

Glu Ser Arg Asn Gly Ala Glu Ile Leu Ile Lys Lys Asn Cys Val Asp
 450 455 460

Ile Ala Lys Glu Ser Asn Ser Lys Ser Phe Val Asn Lys Tyr Tyr Gln
 465 470 475 480

Ser } (*) [Leu Ile Glu Ile Asp Glu Ala Thr Ala Gln Lys Ile Ile
 485 490 495

Lys Glu Ile Lys } (*) [Leu Leu Leu Ile Arg Glu } (*) [Thr Lys Leu Leu
 495 500 505

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500
Ile } * { Arg Ser Ala Ile Phe Asn } * { Arg Asn Lys Ser } * { Thr Lys }
515 520 525
new SEQ ID NO.
505
new SEQ ID NO.
510
new SEQ ID NO.
Val Arg Gln } * { Lys Ile Gln Thr Leu Val Lys Ile Leu Arg Lys Glu
530 535 540
new SEQ ID NO.
Lys Lys Thr Ser } * { Gln Lys Lys Lys } * { Gly Asn Lys } * { Asn Glu }
545 550 555 560
new SEQ ID NO.
Tyr Arg Ser Glu Glu Ile Lys Asp Leu Phe Phe Ser Ile Ile Tyr } *
565 570 575
new SEQ ID NO.
{ Lys Glu Gly Phe Trp Gly Phe Gly Val Leu Gly }
580 585

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Pro Lys Pro Gln Asn Pro Lys Thr Pro Ile Lys Lys Glu Lys Ile Glu
1 5 10 15
Val Val * Lys * Asn Ile Ile Pro Ala Gln Met Glu Met Asp Ile
20 25 30
Asp Leu Asp Asp Ile Glu Asn Leu Leu Pro Asn Thr Phe Asn Lys Tyr
35 40 45
Ser Ser Ser Cys Ser Asp Lys Lys Gly Cys Lys Thr Leu Lys Ser Gly
50 55 60
Ser Lys Ser Pro Ser Leu Thr Ile Pro Lys Leu Gln Lys Gln Leu Glu
65 70 75 80
Phe Tyr Phe Ser Asp Ala Asn Leu Tyr Asn Asp Ser Phe Leu Arg Lys
85 90 95
Leu Val Leu Lys Ser Gly Glu Gln Arg Val Glu Ile Glu Thr Leu Leu
100 105 110
Met Phe Lys * Asn Gln Val Met Arg Ile Ile Leu Phe Phe Arg Ser
115 120 125
Leu Leu Lys Glu His Tyr Gly Glu Asn Tyr Leu Ile Leu Lys Gly Lys
130 135 140
Gln Phe Gly Leu Phe Pro * Pro Thr Met Met Ser Ile Leu Asn Ser

same error - This type
of error
appears
throughout
listing.
Please edit
all
sequences
having this
error

08/974584

145				150					155					160	
Tyr	Glu	Asn	Glu	Ser	Lys	Asp	Leu	Asp	Thr	Ser	Asp	Leu	Pro	Lys	Thr
				165					170					175	
Asn	Ser	Leu	*	Asn	Ala	Arg	Lys	Ser	Leu	Ile	Ile	Glu	Gln	Gln	Lys
			180					185					190		
Asn	Leu	Leu	His	Leu	Leu	Phe	Val	Trp	Val	Leu	Leu	Gln	Leu	Phe	*
		195					200					205			
Val	Ser	Thr	Val	Asn	Ser	Arg	Val	Leu	Arg	Gln	Leu	Lys	Lys	Leu	Phe
	210					215					220				
Thr	Thr	Glu	Gly	Ile	Ala	Val	Leu	Lys	Val	Leu	Met	Cys	Met	Pro	Leu
225					230					235					240
Phe	Cys	Glu	Leu	Ile	Ser	Asn	Ile	Leu	Ser	Gln	Phe	Asn	Gly	*	Leu
				245					250					255	
*	Lys	Gln	Thr	Lys	*	Thr	Met	Gln	Val	*	Trp	Asn	Ile	Arg	*
			260					265					270		
Ile	Leu	Trp	Asp	Lys	Cys	Thr	Leu	Asn	Leu	Tyr	Trp	Ile	Leu	Lys	Ala
		275					280					285			
*	Ile	His	Arg	Met	Leu	*	Arg	Leu	Ile	*	Leu	Thr	Thr	Asp	Tyr
	290					295					300				
Leu	Phe	*	Leu	Leu	Leu	Leu	Ile	Ser	Tyr	Ile	Phe	Lys	Arg	Ser	Arg
305					310					315					320
Arg	Asn	Glu	Lys	Lys	Thr	Lys	Glu	Arg	Asp	Phe	Lys	Ile	Cys	*	Phe
				325					330					335	
Phe	Cys	Asn	Arg	Asn	*	Gln	Gln	Glu	Tyr	*	Gln	Arg	Lys	Arg	Arg
		340						345					350		
Arg	Ala	Ile	Thr	Ile	Leu	Ile	Leu	Lys	Asp	Phe	Lys	Asn	Ser	Arg	*
		355					360					365			
Glu	Arg	Tyr	Ile	His	*	Asn	Ser	Tyr	Ile	Ile	Val	Phe	His	Phe	Thr
	370					375					380				
Ala	Val	Ile	Phe	Phe	Tyr	Leu	Asn	Asn	Ile	Phe	*	Leu	Ala	Gly	Ser
385					390					395					400
Lys	Lys	Tyr	Gln	Ile	Arg	Glu	Ala	Leu	Asp	*	Gly	Asn	Leu	Ala	Tyr
			405						410					415	
Ser	His	Ser	*	Ile	Asp	Leu	His	Ile	Ser	Asn	Thr	Met	Ile	Arg	Lys
			420					425					430		
Gln	Gln	Ser	Ser	Val	Leu	Lys	Ile	Val	Leu	*	Gly	Leu	Asn	Phe	*
		435					440					445			
Ser	Gln	Glu	Met	Glu	Pro	Lys	Ser	*	Ser	Lys	Arg	Ile	Ala	Ser	Ile

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450

455

460

Leu Gln Lys Asn Arg Thr Leu Asn Leu Ser Leu Ile Ser Ile Thr Asn
 465 470 475 480

Leu Asp * Leu Lys Arg Leu Thr Arg Gln Leu His Arg Arg Ser Leu
 485 490 495

Lys Lys * Ser Asn Phe Tyr * Leu Glu Asn Lys Leu Asn Tyr *
 500 505 510

Tyr Arg Asp Gln Arg Ser Ser Ile Asp Glu Ile Lys Ala Glu Leu Lys
 515 520 525

Leu Asp Asn Lys Lys Tyr Lys Pro Trp Ser Lys Tyr * Gly Arg Lys
 530 535 540

Arg Arg Pro Val Ser Lys Arg Lys Asn Lys Ala Ile Asn Lys Met Ser
 545 550 555 560

Thr Glu Val Lys Lys * Lys Ile Tyr Phe Phe Gln * Phe Ile Glu
 565 570 575

Lys Arg Gly Phe Gly Val Leu Gly Phe Trp
 580 585